Mutant-specific oligonucleotide primers used for mutant number 1. Mutated nucleotide underlined.

Bet v 1 sense	5'-	${\tt AATTATGAGACTGAGACC\underline{A}CCTCTGTTATCCCAGCAGCTCG}$	-3 '
Bet v 1 non-sense	3'-	${\tt TTAATACTCTGACTCTGG\underline{T}GGAGACAATAGGGTCGTCGAGC}$	- 5 '
sense primer	5 '	TGAGACC <u>C</u> CCTCTGTTATCCCAG	-3 '
non-sense primer	3 ' -	ATACTCTGACTCTGG <u>G</u> GGAGAÇA	-5'

Oligonucleotide primers for site directed mutagenesis of Bet v 1 (No. 2801).

all	sense	1: 183BV, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4:186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3 _A	sense	6: 188Bv, 23-mer 5'-AACATTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 1918v, 23-mer 5'-AGCIGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 19(Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv. 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

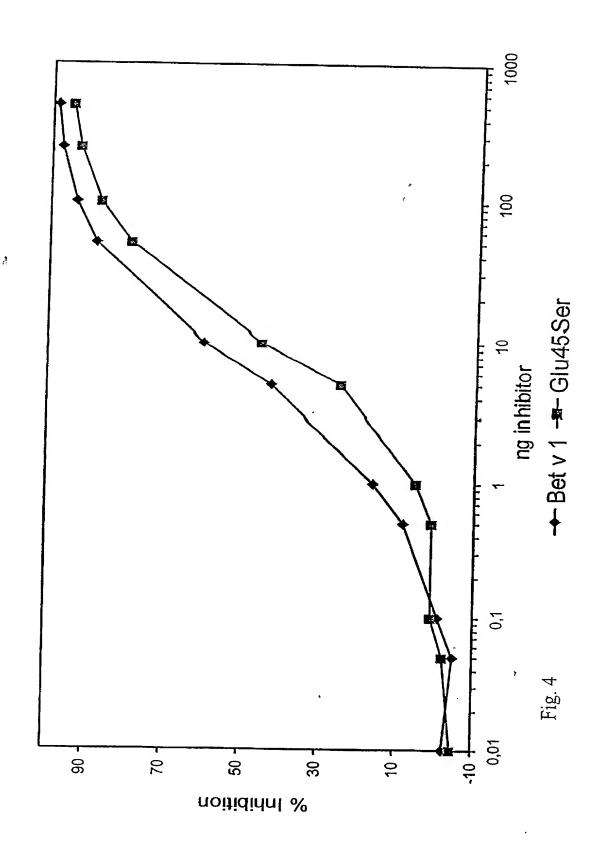
Overview of all Bet v 1 mutations

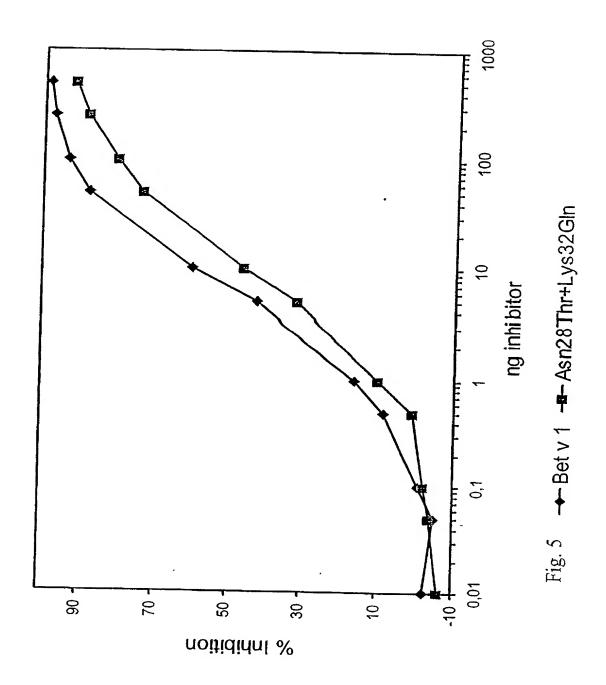
									1 (A-C)									
GG	CTC	TT	AAT	TAT	rga	GAC	TGA	GAC	CAC	CTC	TGT.	rat	ccc	AGC	4GC	TCGI	CIY	STT	CAAG	60
G	v	F	N	Y	E	т	E	T	T -3	PS	v	1	P	A	A	R	r	F	κ	20
				9 (A-	-G)		2	(A-	C) :	2 (A	-C)									
GCC	111	YTA	CT	TG <u>A</u> T	GG(CGA	TA <u>A</u> C	CI	CTT	rcc	A <u>A</u> AG	GT	rgC:	ACCC	CA	AGCC	'ATT	AG	CAGT	120
A	F	I	L	D-G	G	Đ	N-7	L	F	₽	K-Ç	v	A	P	Q	A	1	s	s	40
		3 (0	A-1	rc)	•	7 (A	እ- ፕር	;)					4	(G-C	:}		6 (GA-	-TC)	
GTT	GAA	AAC	AT	r <u>ga</u> a	GG	/AA	rgga	GGC	CCI	'GG/	AACC	ATT	'AAC	:AAG	ATC	CAGC	TTT	CCC	<u>ga</u> a	180
v	E	N	I	E-S	G	N-3	S G	G	₽	G	T	1	K	K-N	I	s	F	P	E-S	60
															5	(CA	-TG)		
GGC	crc	CCT	TTC	CAAG	TAC	GT	Baag	GAC	AGA	GTI	GAT	GAG	GTC	GAC	CAC	<u>'A</u> CA	AAC	TTC	AAA	240
G	L	₽	F	K	¥	V	ĸ	D	R	v	D	E	v	D	H	T-A	N	F	ĸ	80
TAC	TAP	TAC	AGC	GTG	ATC	GAC	GGO	GGI	ccc	ATA	GGC	GAC	ACA	TTG	GAG	AAG	ATC	TCC	AAC	300
Y	N	Y	ន	V	I	£	G	G	P	I	G	D	Ŧ	L	E	ĸ	I	S	N	100
10 (BAG	-CA	C)		8	(CC	C-T	GG)												
GAG	ATA	AAG.	КТA	GTG	3CA	ACC	CCT	GAT	GGA	GGA	TCC	ATC	TTG	AAG	ATC	AGC	AAC	AAG	TAC	360
E	I	ĸ	I	v	A	T	P-G	D	.G	G	ន	r	L	ĸ	r	s	N	к	Y	120
CAC	ACC!	AAA	GGT	GAC	CAT	GAG	GTG	A AG	GCA	gag	CAG	GTT.	AAG	GCA	4GT	AAA	SAA	ATG	GGC	420
н	T	ĸ	G	D	н	£	v	к	A	E	Q	v	κ	A	s	ĸ	E	м	G	140

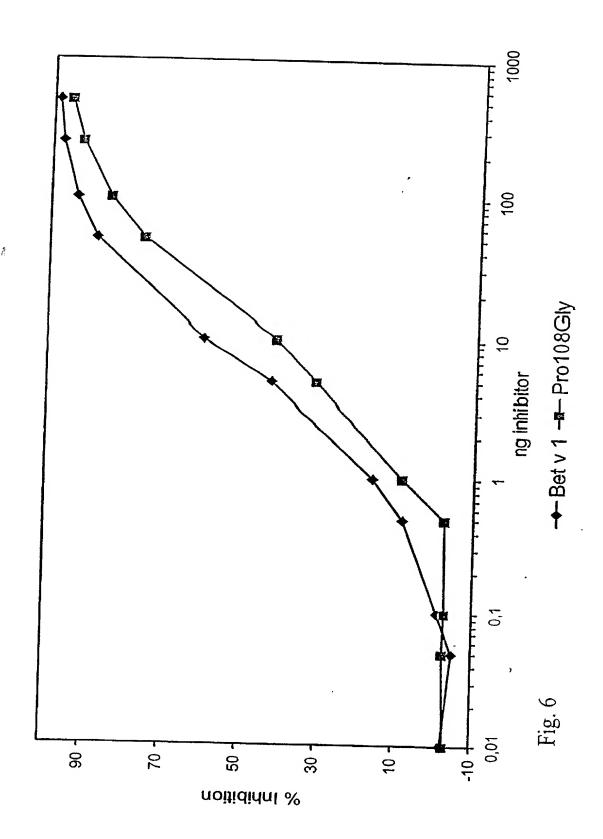
 ${\tt GAGACACTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAACTAA}$

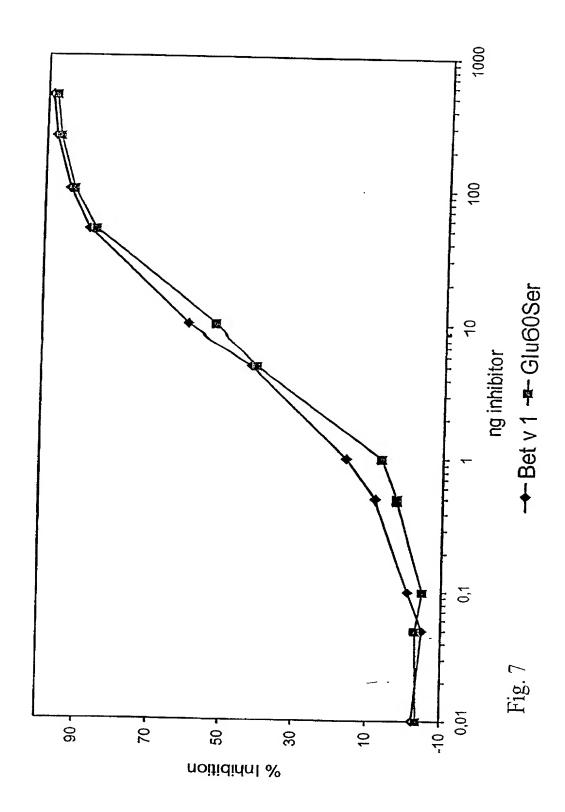
E T L L R A V E S Y L L A H S D A Y N stop

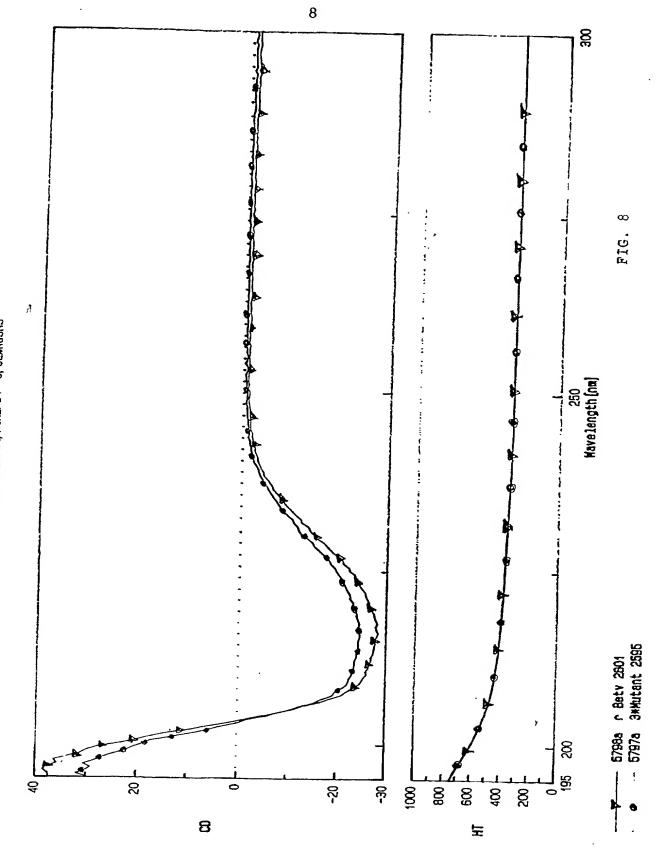
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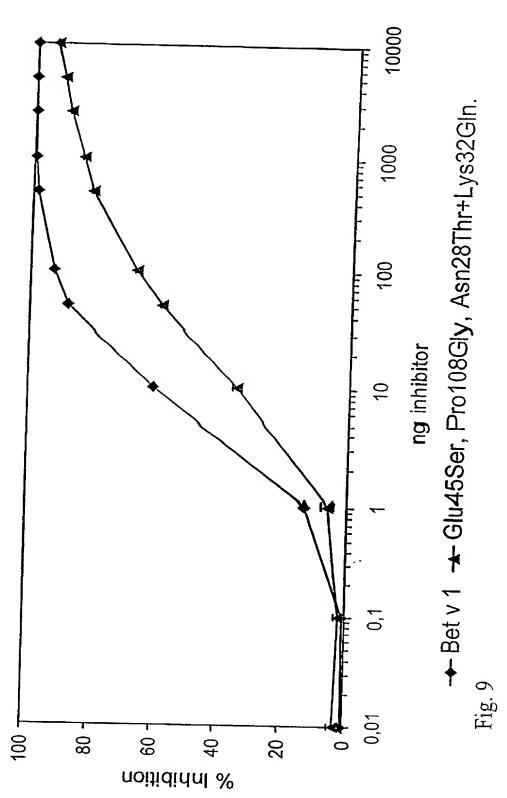












Conserved residues among Vespula antigen 5

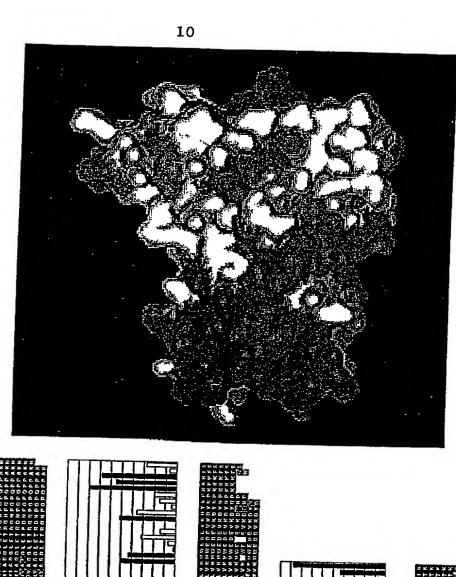
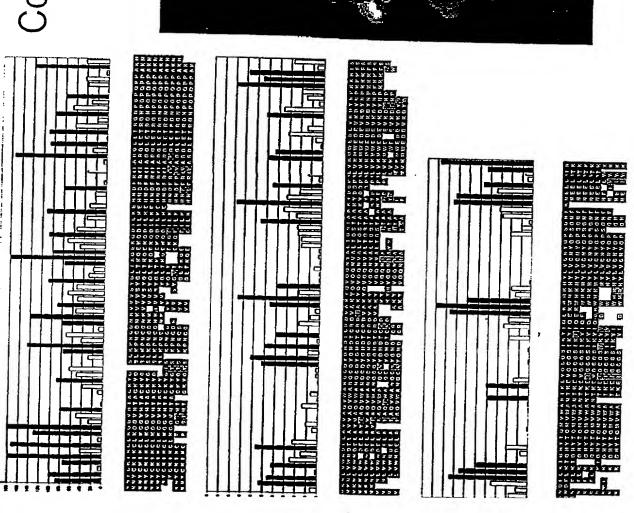


Figure 10.



Ves v 5 mutant 1 (K72A) Ves v 5 sense 5 - ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA -3 -Ves v 5 non-sense 3 - TGGTGTCGGAGGTCGCTTCTTATACTTTTTAAACCATACCT -5 ' sense primer 5 -CCAGCGGCTAATATGAAAAAT -31 non-sense primer 3'--51 **GTCGGAGGTCGCCGATTATAC** Ves v 5 mutant 2 (Y96A) Ves v 5 sense 5 - GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG -3 -Ves v 5 non-sense 3 - CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC -5 sense primer TGTCAAGCTGGTCACGATACT -3~ non-sense primer 3 ~ TTAGTTACAGTT<u>CG</u>ACCAGTG -51

Oligonucleotide primers for site directed mutagenesis of ${\tt Ves\ v\ 5.}$

all sense 1: XhoI start, 38-mer:

Ecori

5 ~- CCGCTCGAGAAAAGAAACAATTATTGTAAAATAAAATG

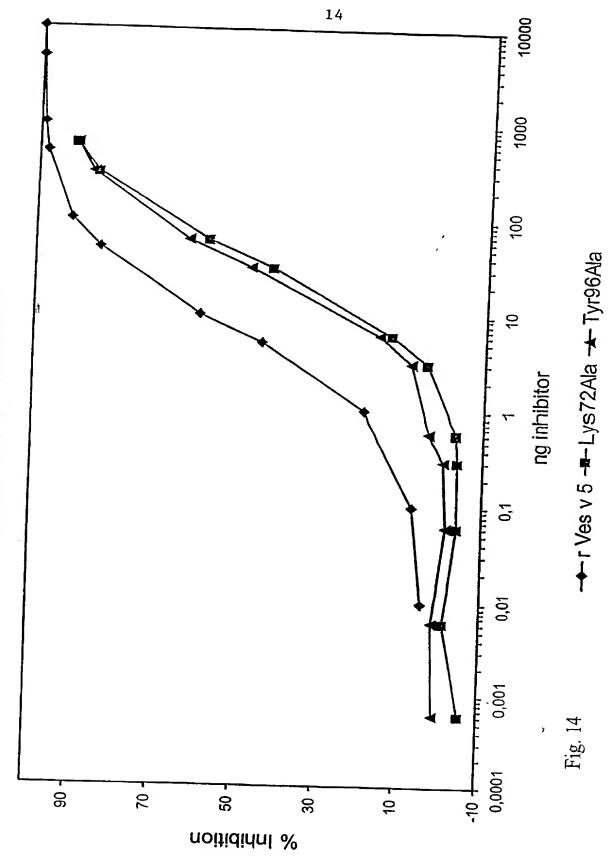
LEKRNNNYCKIK Kex2 cleavage site amino terminus of Ves v S

1	sense	1: K72As	21-mer	5´-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5~-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5´-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5~-GTGACCAGCTTGACATTGATT
Å				
all	non-sense	7: CT-pPIC	ZαA, 21-mer	5~ATTCATCAGCTGCGAGATAGG

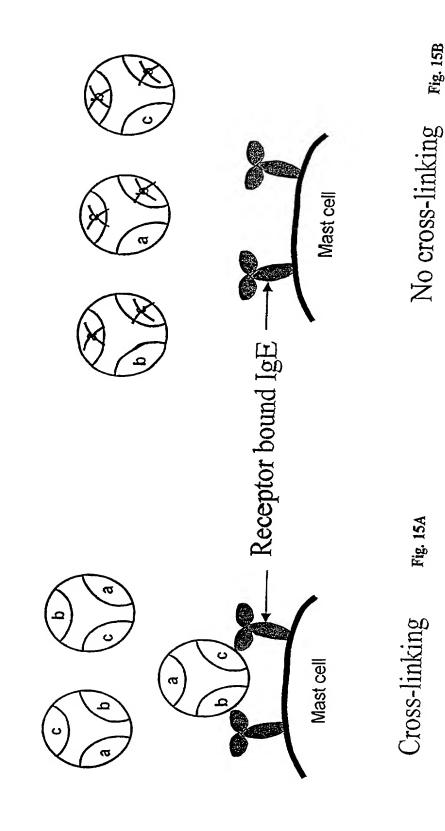
THE RESIDENCE OF THE PARTY OF T

Overview of Ves v 5 mutations

1	AA	'AA	TTA:	r i g'	TAA	AAT	AAA	ATG'	rtr	SAA	AGG/	AGG'	rgt	CCA:	rac	TGC	CTG	CAA	ATA	TGGA	60
1	N	N	Y	С	ĸ	I	ĸ	C	L	К	G	G	v	H	T	A	C	K	Y	G	20
61	AGT	יריי	מ מח	אכריי	ממבי	ቦጥር	ייניניי	י ממיו	א מיז	ኒርኒጥን	ረም የ	፤ርጥ)	<u>ነ</u> ጥር ነር	ימיניי	ויממי	тст	ם א כינ	ממב	מטמ	AGAG	120
21			K									v				L			0		40
21	٥	Į,	IC	F	IV	C	G	14	10	•	٧	V	3	1	G	n	1	K	Q	E	4.0
121	AAA	CA	AGAC	CATO	CTTA	AAA	3GAC	CAC	CAAC	GAC	TT	raga	CAF	LAAZ	AT.	rgcz	\CG	AGG!	TT	EGAG	180
41			D		L								Q			A					60
												11	K72	AI ((AAC	G-GC	T)				
181	ACI	'AGF	GGI	'AA'	rcci	GGA	LCC#	CAC	CCI	CCA	GCG			• •	•		-	GTA	TGO	FAAC	240
61					P								-							N	80
								~													
																			•	-GC)	
241	GAC																GG1	CAC	GA?	CACT	300
81	D	E	L	A	Y	V	A	Q	V	W	A	N	Q	C	Q	Y	G	H	D	T	100
201	ma a	200	CI N m	com x	COX	***	01 N 07	(A)	ć.mr	~~~	~~~	70 70 60	com n	000	ת ונאדא	202	001	17.00	·	ıaam	260
301																					360
101	С	R	D	v	A	K	Y	Q	V	G	Q	N	V	A	L	T	G	S	T	A	120
361	GCT	AAA	TAC	GAT	GAT	CCA	GTT	AAA	CTA	GTT	AAA	ATG	TGG	GAA	GAI	GAA	GTG	AAA	GAT	TAT	420
121	_		_						-	_			W			E	v		D	Y	140
421										-									CAA	ATG	480
141	N	P	K	K	K	F	S	G	N	D	F	L	K	T	G	H	Y	${f T}$	Q	M	160
481	Contra	TV-1/-	~~m	**~	3.00	**~	~ »	~~~	aam	mvam.	~~*	3 A M	2012	***	60 Z C	13 TW	~~~	03 O	N 7 7	maa	540
161												AGT S		AAA K		AII I	CAA O		AAA K		180
101	٧	W	A	TA	1	K	E	Y	G	•	G	3	_	K	1	-	V	E	K	N	100
541	CAC	ממה	ርግ አጥ	ጥአር	منسب	ርያጣኘሽ	ሞረነጥ	አጸጥ	ጥ አጥ	יעבט	~~~	አርር	CCA	አአሮ	لمنعية	מממ	አአጥ	(Z) / (Z)	ርል አ	بيعيب	600
181																K	N		-	L	200
	••		**	•		•	_		-	•	-	_	-	•-	-			_	_	_	- * *
601	ТАТ	CAA	ACA:	AAG'	TAA																612
201																					204
						-															



Effect of point mutations in dominating IgE epitopes hypothetical model with 3 epitopes



DNA SEQUENCE

Der p 2 (DNA sequence referred to in notes in accession No. P49278 SWISSPROT)

ORIGIN

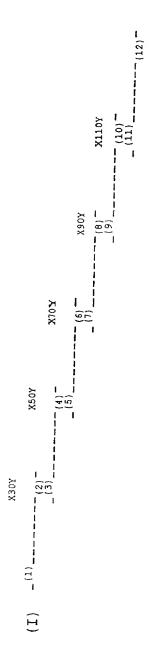
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61	cattcaaaat gatgtacaaa attttgtgtc tttcattgtt ggtcgcagcc gttgctcgtg
121	atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagttttg gtaccaggat
181	gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccgttt
241	togaagocaa coaaaacaca aaaacggota aaattgaaat caaagootca atcgatggtt
301	tagaagttga tgttcccggt atcgatccaa atgcatgcca ttacatgaaa tgcccattgg
361	ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat
421	ctgaaaatgt tgtcgtcact gttaaagtta tgggtgatga tggtgttttg gcctgtgcta
481	ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa tttattgatt ttgtaatcac
541	aaatgattga ttttctttcc aaaaaaaaaa taaataaaat tttgggaatt c
	5 - 5

AMINO ACID SEQUENCE

Der p 2 (Accession No. P49278 SWISSPROT; includes signal peptide 1-17)

- mmykilclsl Ivaavardqv dvkdcanhei kkvlvpgchg sepciihrgk pfqleavfea nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen vvvtvkvmgd dgvlacaiat hakird 1 61
- 121

Figure 17



(II) -(1)-----X30Y-----X50Y-----X70Y----X90Y----XI10Y----(12)-

Lines represents DNA sequences.

Numbers in parentheses above lines represents sense oligonucleotide primers: (1), (3), (5), (7), (9), (11).

Numbers in parentheses below lines represents anti-sense oligonucleotide primers: (2), (4), (6), (8), (10), (12).

Notation X (position) Y represents mutations.

(1) Represents the sense oligonucleotide primer accommodating the protein N-terminus. (12) Represents the anti-sense oligonucleotide primer accommodating the protein C-terminus.

(A16P, N28T, K32Q, K103T, P108G, L152K, A153G, S155P) DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations. 372BVa CAGACTAATTCGACGTCGGTACCC CAGTCGcggTGCTGGGATAACAGA CACTATGGTTATCTCGTTGGAGAT GAGATAaccATAGTGGCAACtggT CCAGCAccgCGACTGTTCAAGGCC 370BVa 369BVs 368BVa 367BVs Bet v 1 (2637) 331pMalc 331 pMalc 368BVa 367BVs 370BVa 369BVs Bet v 1 (2628) (Y5V, E45S, K65N, K97S, K134E) 366BV (a) 365BV (s) DNA template: Bet v 1 (2589) carrying the Y5V mutation. 364BV (a) 363BV (s) 362BV (a) 361BV (s) 189BV (a) 188BV (s) Figure 18 331 pMalc (s)

372BVa:TTACTGAATTCATTAGTTGTAGGCATCcggGTGgcctttGAGGTA

CAGACTAATTCGAGCTCGGTACCC

O

331pMa1

CACGTAGTTGAAAGGGAGGCCTTC

362Bva 361BVs

189BV 188BV 364Bva 363BVs

TTTCCTGAAATGTTTTCAACACT
AACATTTCAGGAAATGGAGGGCC

GGAGATGCTCTCCAATGTGTCGCC GGAGAGCATCTCCAACGAGATAAA ACTTGCTTCAACCTGCTCTGCCTT CAGGTTGAAGCAAGTAAATG

GCAGGTCGACTCTAGAGGATCCAT

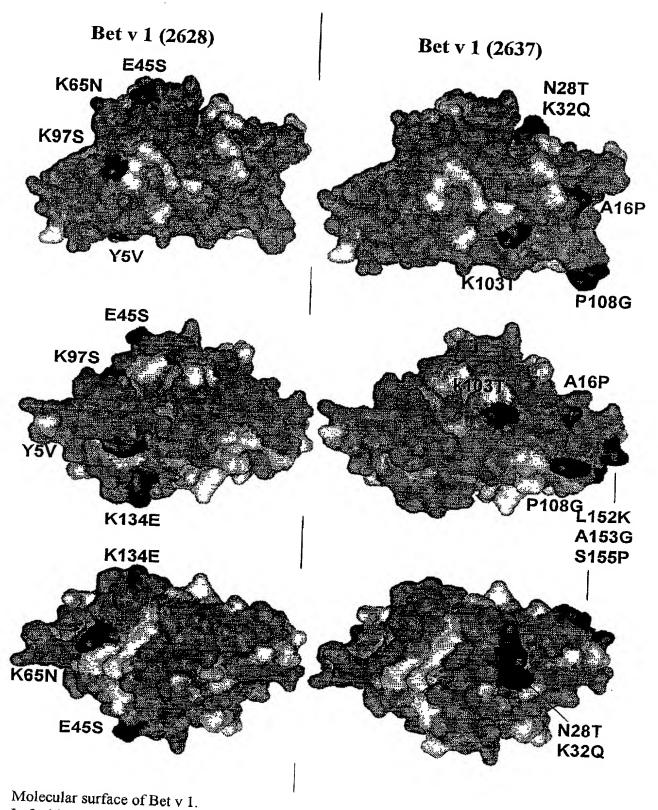
Ö

332pMal

366Bva

365BVs

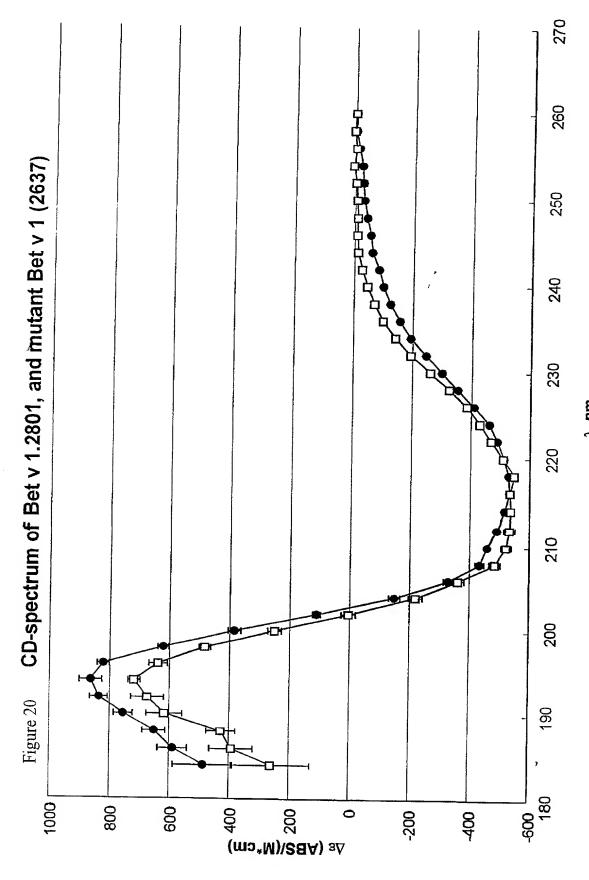
TTTCAACTACGTGAAGGACAGAGT



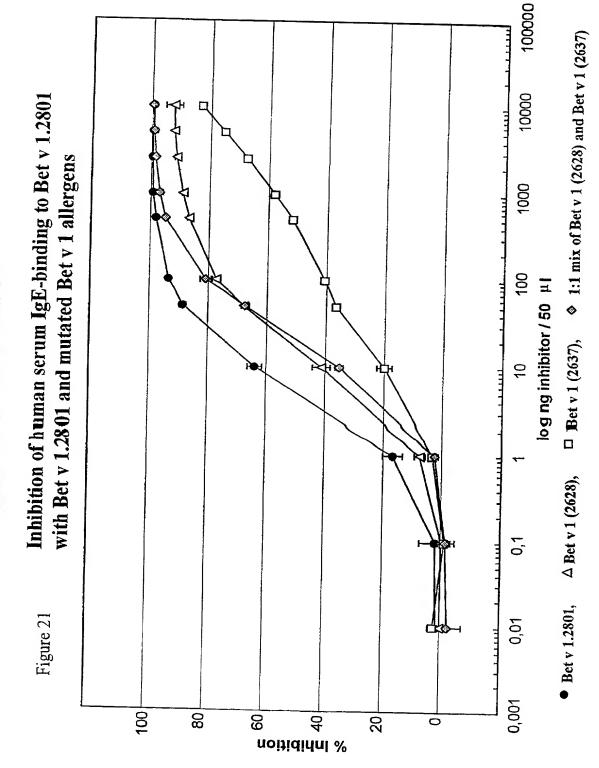
Left side: Bet v 1 (2628), Right side: Bet v 1 (2637)

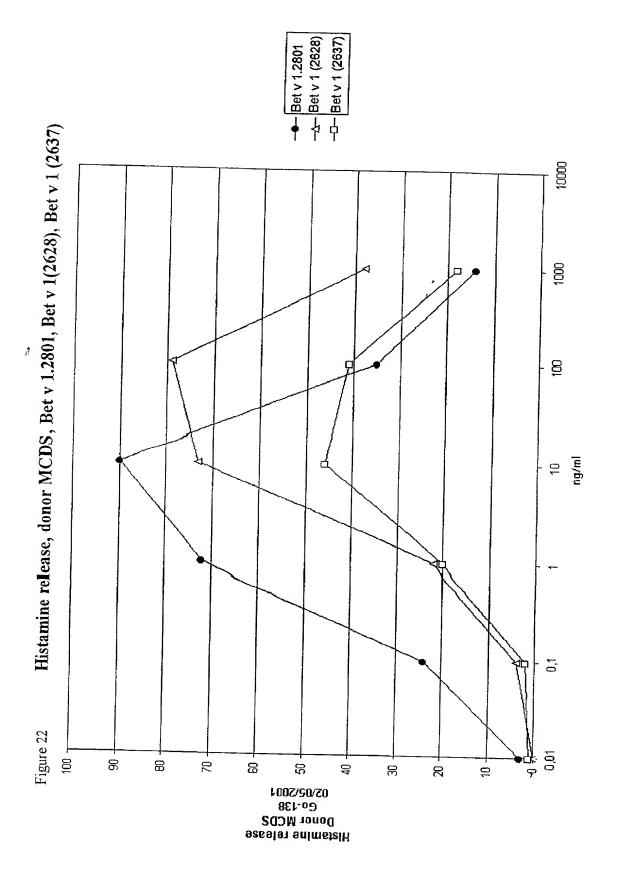
Grey: Backbone + amino acids 95-100% conserved among Fagales Black: Introduced point mutations.

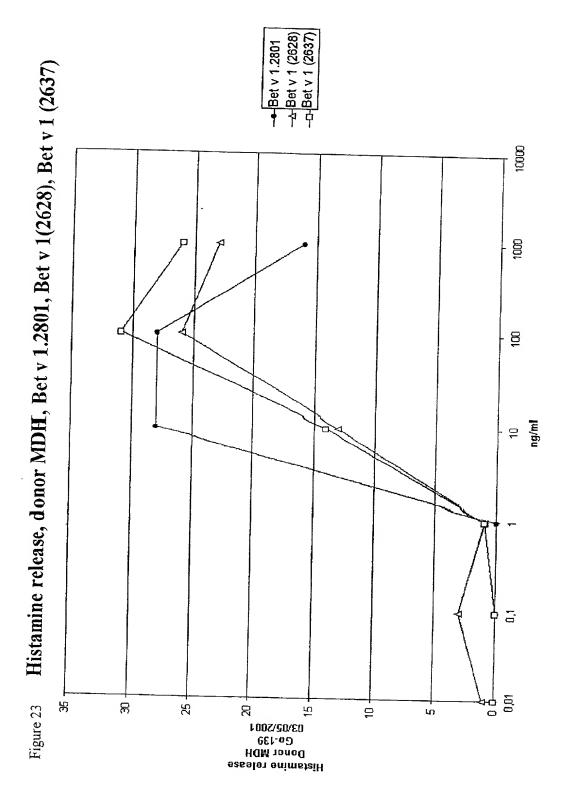
Figure 19

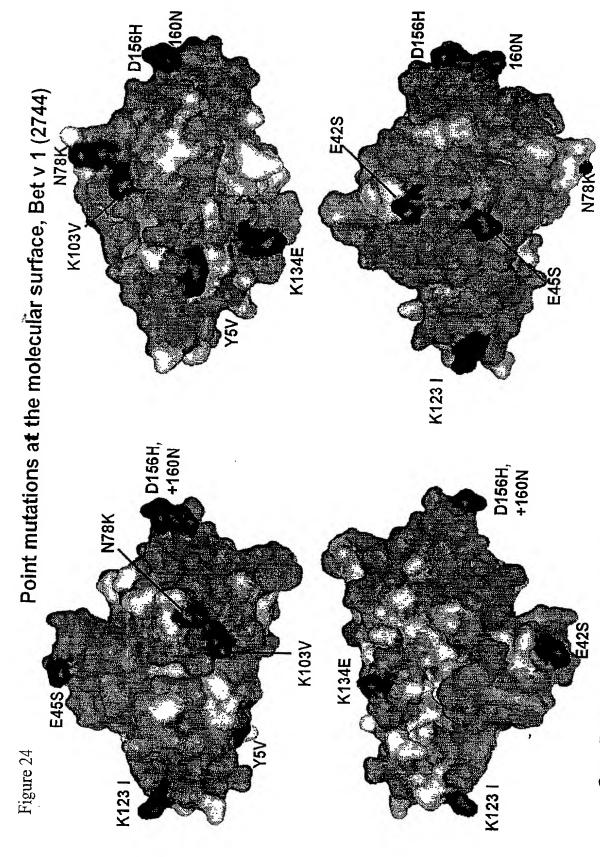


λ**, nm** CD-spectrum of Bet v 1 (2637), open squares, and the CD-spectrum of native folded Bet v 1.2801, closed circles, both obtained at 20 °C

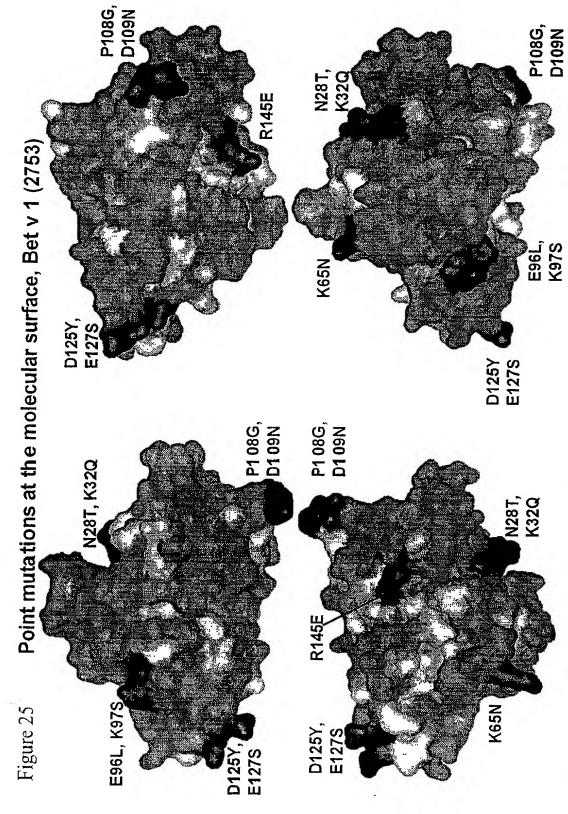






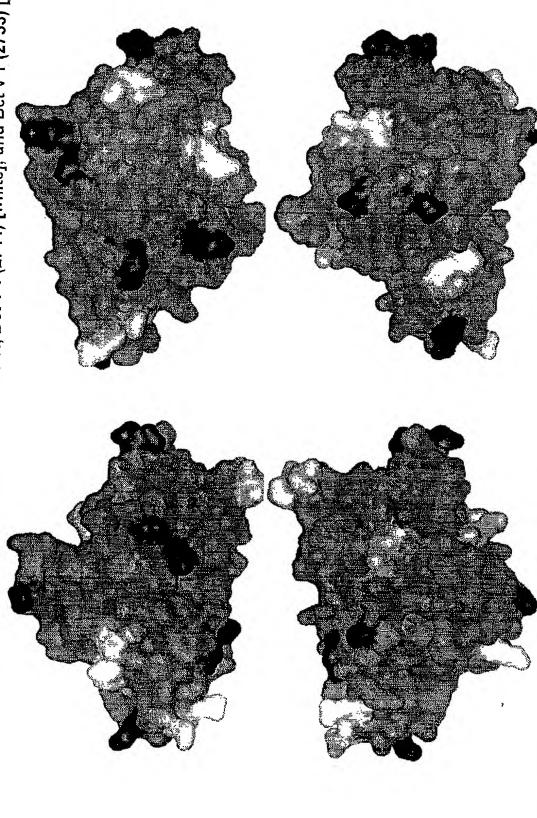


Grey: Back bone + Amino acid residues 95-100% conserved among Fagales, Black: Point mutations



Black: Point mutations Grey: Back bone + Amino acid residues 95-100% conserved among Fagales,

Distribution of point mutations at the molecular surface of, Bet v.4 (2744) [white], and Bet v 1 (2753) [Black]

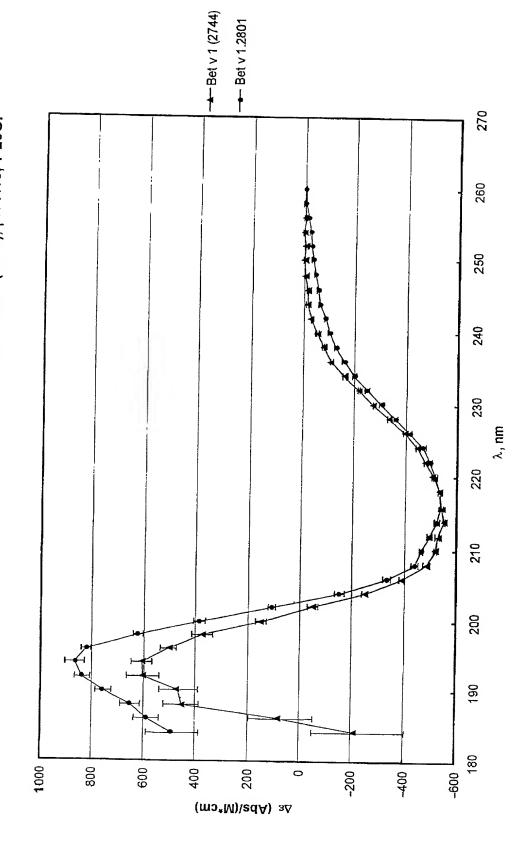


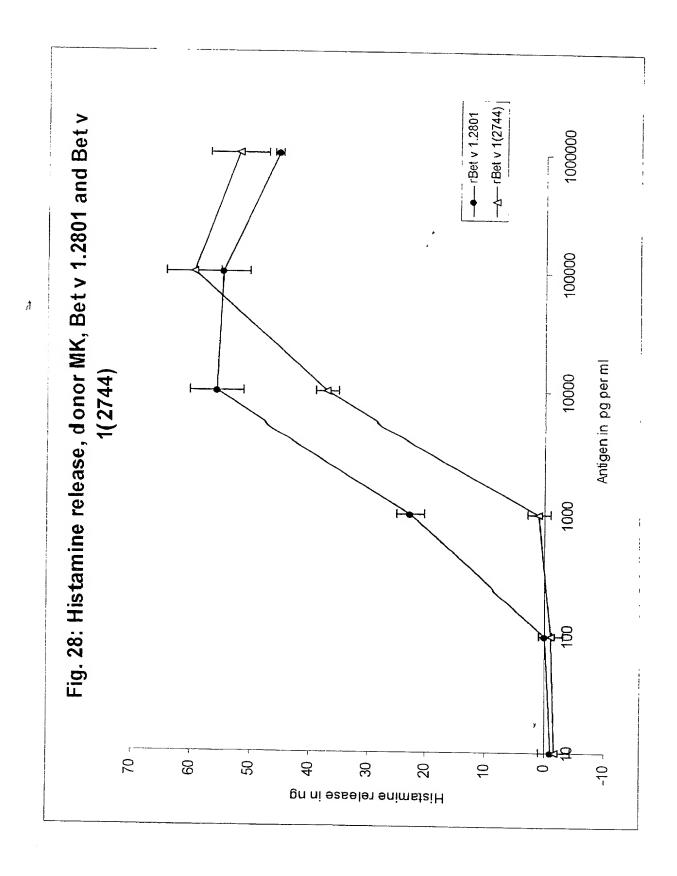
Grey: Molecular surface; amino acid residues 95-100% conserved among *Fagales*Black: Mutations (Y5V, K134E), (E42S, E45S), (N78K, K103V), K123 I, (D156H, +160N)

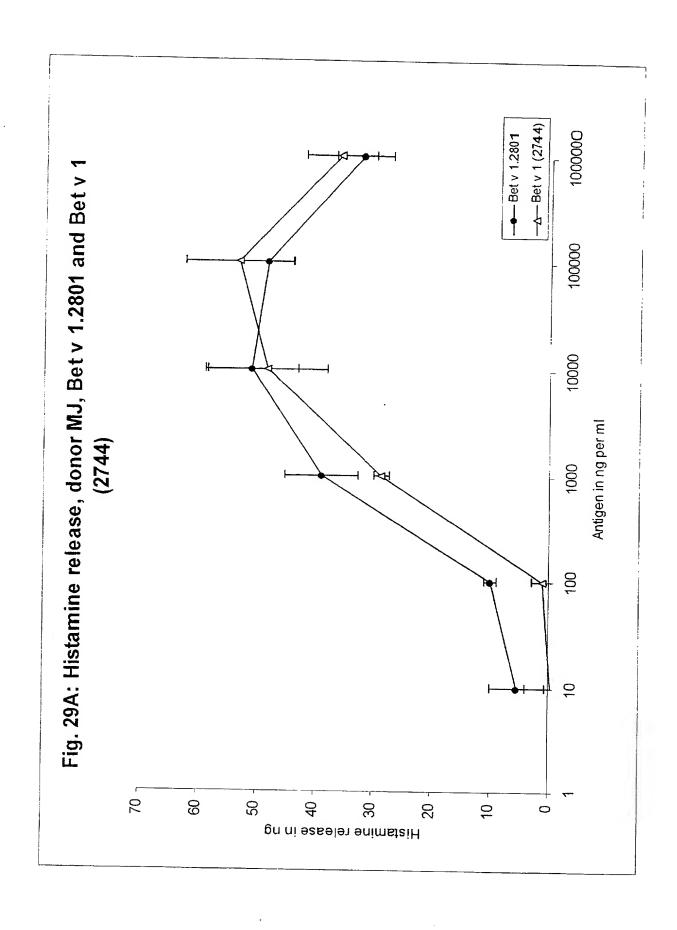
White: Mutations (N28T, K32Q), K65N, (E96L, K97S), (P108G, D109N), (D125Y, E127S), R145E

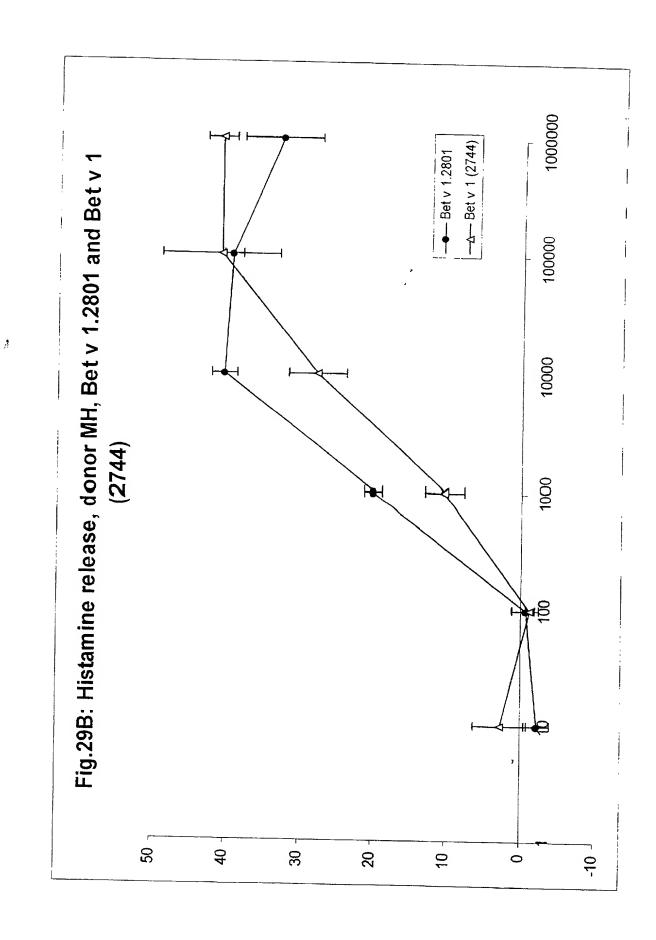
Figure 26

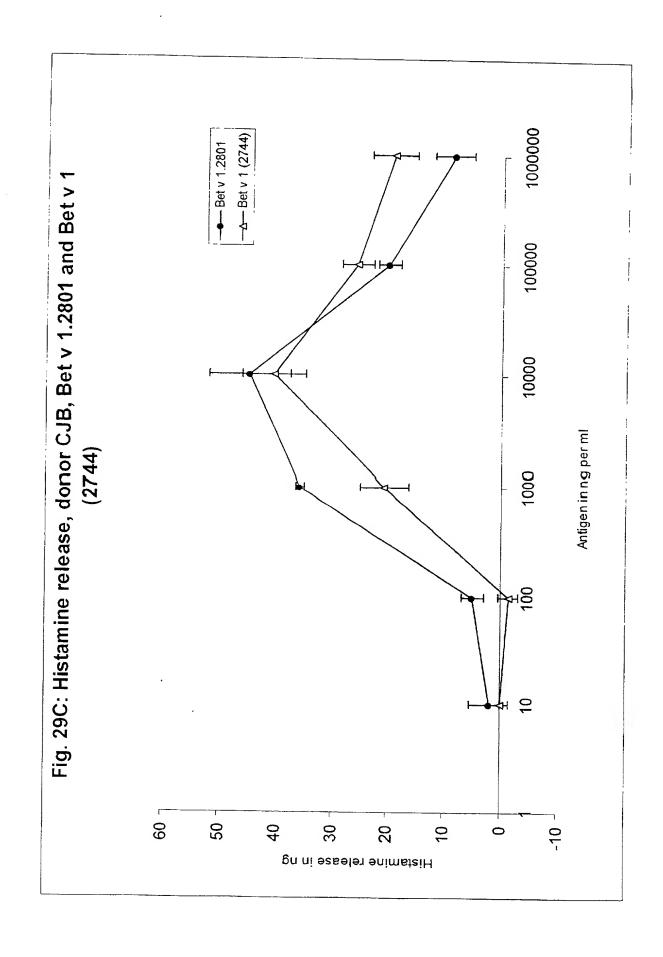
Figure 27 Circular dichroisme spectra of Bet v 1.2801 and mutant Bet v 1(2744), pH 7.13, T 20C.



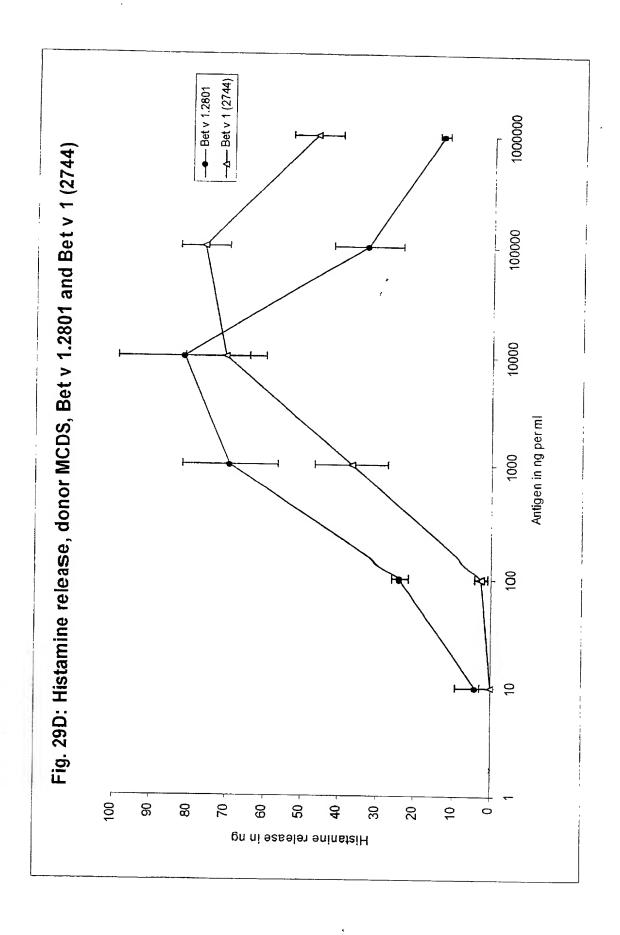


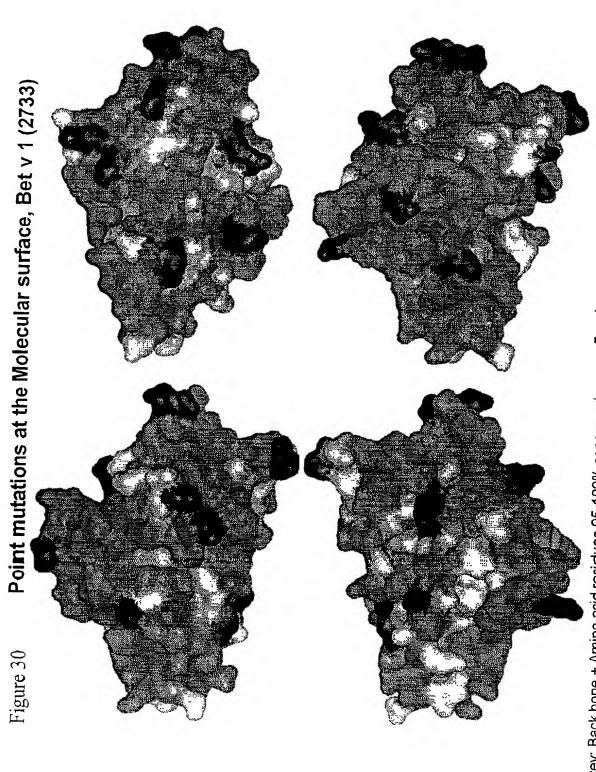






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The state of the s

Grey: Back bone + Amino acid residues 95-100% conserved among Fagales, Black: Point mutations: Y5V, N28T, K32Q, E45S, K65N, N78K, K97S, K103V, P108G, K134E, R145E, D156H, +160N

.

Figure 31

Oligonucleotide primers for site-directed mutagenesis of Der p 2

				Xho I
K6∧	sense	OB43	42-mer	5'-CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC-3'
	anti-sense	OB28	39-mer	Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTT,TAGCATGAGTTGC- 3'
K15E	sense	ОВ44	67-mer	3° -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTTGG-3°
	anti-sense	OB28	39-mer	Xba1 5'-CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
H30N	sense	OB46	54-mer	Lpn I 5' -CGG <u>GGTACC</u> AGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC 3'
	anti-sense	OB28	39-mer	Xba1 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC-3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC-3'
H74N	sense	OB49	32-mer	Sph I 5' -CATG <u>GCATGC</u> AATTACATQAAATGCCCATTGG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
K82N	sense	OB50	50-mer	5'-CTAC <u>GCATGC</u> CATTACATGAAATGCCCATTGGTT AAT GGACAA CAATATG-3'
	anti-sensc	OB28	39-тег	Xbu I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'

,

10 2 0		P V V V V V V V V V V V V V V V V V V V	PER SECTION OF THE SECTION OF THE SECTION OF		12 0
1 DERP2-AI K-G Dern 2	Derp 2	3 UEC JENTA Der 12 000855 10 B61241 Der 12 661241 11 IAHK Der 12 PDB 12 OSG30 Eurm 2 0101 OSG430 14 OST222 Eurm 2 0102 OST222	1 DERPZALK-G Der p 2 2 DERP 2 CDNA Der p 2 3 DERPZ-ISO(101 :Der p 2 4 DERPZ-ISO(102 Der p 2 5 DERPZ-ISO(104 Der p 2 6 DERPZ-ISO(104 Der p 2 7 DERPZ-ISO(104 Der p 2 7 DERPZ-ISO(104 Der p 2	10 DEF 2 DEF 2 DEF 3 DEF 9 DE 9 DE 9 DEF 2 DEF 8 DEF 10 DEF 12 Q00665	1 DERPZ-ALK-G Der p 2 2 DERP 2 CDNA Der p 2 3 DERPZ-ISO101 Der p 2 4 DERPZ-ISO101 Der p 2 5 DERPZ-ISO101 Der p 2 5 DERPZ-ISO102 Der p 2 6 DERPZ-ISO103 Der p 2 7 DERPZ-ISO103 Der p 2 8 149V Der p 2 9 DEF 2 DERFA Der f 2 9 DEF 2 DERFA Der f 2 11 1441K Der f 2 12 A61501 13 096430 Eur m 2 0101 096430 14 09722 Eur m 2 0102 09722

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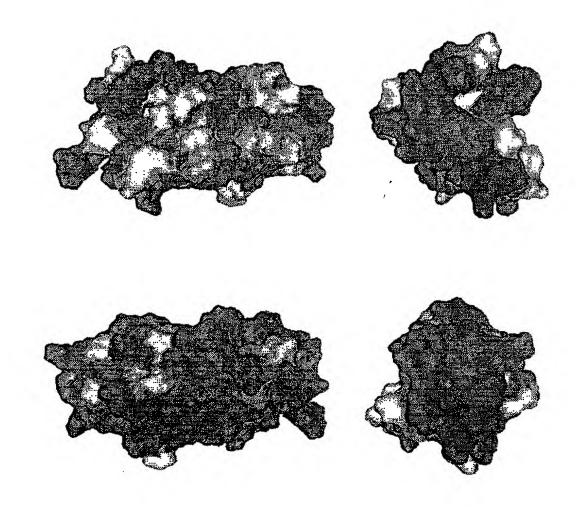


FIG. 33: Der p 2

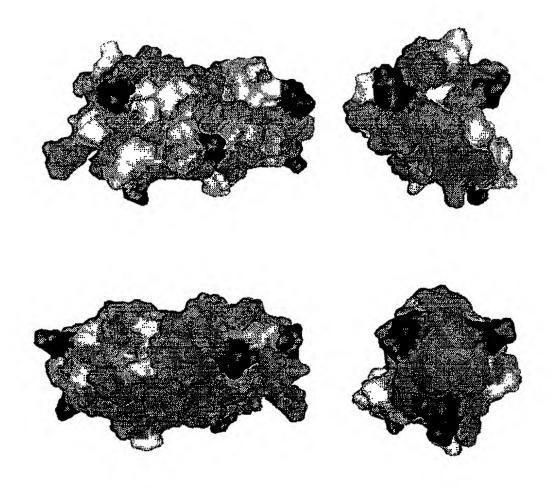


FIG. 34: Der p 2 mutant

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1 3 0 1 3 0 2 4 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
1 2 0	1 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
C C R R P P R C C C C C C C C C C C C C	1.7.0 1.7.0 1.7.0 1.0.0 1.	
1	HE WAS TO SEE THE SEE	N.M. I. F. E. V. D. V. V. I.
P. H. G. F. T. L. G. H. H. B. V. V. G. F. T. L. G. H. H. B. V. V. G. F. T. L. G. G. H. G. V. G. F. T. L. G. G. H. G. V. G. F. T. L. G. G. H. G. V. G. F. T. L. G. G. H. G. V. G. F. T. L. G. G. H. G. V. G. F. T. L. G. G. H. G. V. G. F. T. C. G. G. H. G. V. G. F. T. C. G. G. V. G. F. T. G. G. V. G. F. G. G. G. G. V. G. F. G. G. G. G. V. G. F. G. G. G. G. V. G. F. G.		2.00 2.10 2.10 W.S. D. H. C.
Der p1 AUX Der p1 AUX Der p1 D	Der pl ALK 7	Der pt ALK Der pt 1 Eurm 1 0101 Eurm 1 0101 Eurm 1 0102 Der f1 Eurm 1
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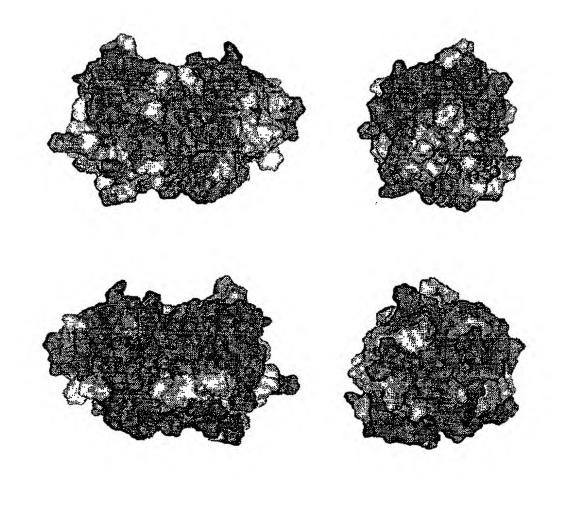


FIG. 36: Der p 1

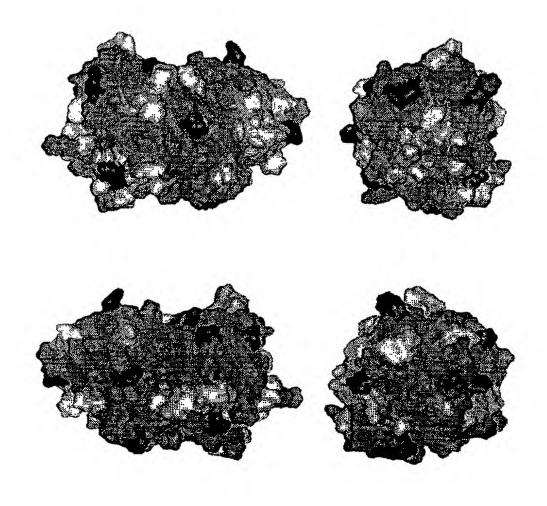


FIG. 37: Der p 1 mutant

FIG. 38A (Phl p 5)

110.0011	111 P 3)							. : -					
				. 2 0		. !		1 0	٠.		;		
1/1081341(081341	PH p 5.0103		M A				LAV	ALL	<i>"</i>	- ".	• , •		-
triO40960 Q40960 sp Q40962 MP5A_PHLPR	Phip5	7.1	- М А	V.H.O.	TYLA	L F	L,A'Y.	ALV	'. · . · .			7 4 7 7	
spiP72286IMP92_POAPR	Pos p 5 (KBG41)	1	A M	VHOY			L A V	ALV	/· î		.,) 1:
spiP22286[MP93_POAPR triO65319iO65319	'Pos p 5 (KBG60) 'Phi p 5	` -j	· KA	A O K A	TIVA	<u>.</u> L.F.	Ė, - į A.	A L V	/	• • • •	• • • • • • •		• • •
tri065320 065320				,					•		: ',	***	:·:ˈ:
140653211065321	PH p 6					. [.		<u>. </u>		[
tr 066318 066318 tr P93467 P93467	PH p 6 PH p 5					EE			1: ::	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;		11.74.1	: 7.7
spiP22284[MP91_POAPR	Poa p 5 (KBG 31)		M D K A	HGAY	KTA	L K	A A S	ÄΥA	PA	E, K [°] F, F	V E Q A	T F D K	N L K
sp[Q40237]MPSB_LOUPR triQ9XF24 Q9XF24	Lol p 58 Lol p 5A		M A	VOKH	A V T	LF		A, L V					
tri098099 098099	Lot p 5C		М А	VQKY	T V A	L.F	LAV	ÀLV	Ŷ.	` ` ` ` `			•
1rj081343j081343 1rj023972j023972	Phl p 5 0206 Hol I 5		М.А.	V.Q.K.Y	T.V.A	Į L.E,	L.A.V	A.L.V	' ·	-			
tri081344j081344	`Phl p 5 0207		- MA	VQKY		L F	LAV	ALV					
1n/AAG42255/AAG42255 1n/AAG42254/AAG42254	Holi5B Poap5		A M A		TÎVÎA		LÎTÎV LÎTÎV	A, L V	· , · ,		·	(· · · · · ·	
11/081342/081342	Phi p 5 0203	S V K.			HRG			GPR					
trjP93466jP93466	Phi p.5		 .	ـــ ــا : إـــا،		A,V		G P R				37:25-	٠,٠,٠
spiQ40963jMP58_PHLPR tdQ9SBE0jQ968E0	Phi p 58 Phi p 5 0204				AAA	AV	PRR	G P R				`:. <u>-</u> }_:	
tr O23971 O23971	Phi p 5.02		-1-1-1		TeleTe			4:	[-]-]	- ": † - , .		, ' ~ '	
epiPS6166(MP53 PHAAO HAAO	Pha a 5.3 Pha a 5.1		- M A	VQKY	TWA		LAV	ALV				• 1-1-1-1-1	
11/004828/004828	Hor v 9	1.1.1.	M.A.H.S	GREH			RRN	L V A	: - 1 - 1				
tr Q39995 Q39996	Hory 6 (30kDa)		ر مر داندا ش				:		1747	-,•;•		٠٠,٠,٠ -	٠.,
	·•····································								.i		-)		
/			1 0		1-1-	2	0				. , , , 3	0	
1/061341/081341	PN p 5.0103		Aire	ALASPIA	9 6 Y	THE S	ATTIES	A A				E RIGHT	
triQ40960 Q40960 sp Q40962 MP5A_PHLPR	Phip 5	1-4:4-5			e C				E		A D	ALC	
spiP22285jMP92_POAPR	Pos p 5 (KBG41)	PAT	i a y	T	APA	AG	Ÿ	300			A	A PARO IN	An
spPZZZ96MP93_POAPR		P		A T BA	PA	AG	Y		A.G.		. A		A 1
14065319(065319 14065320(065320	Phip5					G			* E		T A	a a s	
11(065321)(065321	Phip5	7-1-7-	-, -, -, -,		- - -	G	11.0		E		AA	P. 4 C. K	A T
14065318J065318 14P93467JP93467	Phip5				7 7 7 7 7	G			E .		A A		A 1
SPIP22284IMP91_POAPR	Pos p 5 (KBG 31)	PPA	S.K.F	A K P A	PKV	A A	Y	a a r	A C	`.· ;	A	e k	NΨ
6p/Q40237[MP5B_LOLPR] 1dQ9XF24[Q9XF24	Loip 5H Loip 5A	- A.T.	P LOSSESSE	A STATE	AA	1.0	AAA	A T	A T	AA.		PSGK AGGK	4
tri0950991095099	Lol p 5C		-, -;			7.0	AAA			A'A	TPAA	GGGK	A 1
triO81343[O81343 triO23972[O23972	Phi # 5 0206				- 8	A	Δ	÷		: ; ; ; ;		A G A	
11/081344 081344	Phi p 5.0207					A	A 6 ()	. A.	AIG.	٠, ٠,١٠٠٠		F 6 1	A. ·
InJAAG47255JAAG42255 InJAAG42254JAAG42254	Holl 58 Posp 5				N		T TYPE	*			A		- P
11/081342/081342	PH p 5.0203					Δ							* Y
inP994661P93466 epiQ40963IMP6B PHLPR	PN p 5					A							
triQ9S8E0jQ9SBE0	PN p 5.0204		-1-1-1-			A	KT U	4.4	A.C.		A.C	A 31 K	A I
1/1023971/023971 10/P56166/MP63_PHAAQ	PN # 5.02 Pha # 5.3					2783	P m	. T.			V P G A	A EXTENSION	and and
HAAO	Phs a 51							RT	P		LPPP	R A R D	KA
14004828 004828	Horv9		- N·I	N F	PVF	NR	TEF	K	Mag.		i i I 🌉		₽ E
1403999[039996	Horys (30kOa)	,.t a * .7.*		.*;;			······································		, ,		i,	, · ·	
		q:	n"	3 4 .	1	a a		1				120	
	*									***************************************		en e	naminimizar
1/j081341/081341 1/j040960/j040960	PH p 5.0103				2								1 A K
EPIO40962IMP5A_PHLPR	Phi p 5 A	JEEP N		4 6 6 5	K KI			(40)4		SURFER	8 (L)	C A Ter	1.0 K
SPIP22295 MP92_POAPR	Pos p 5 (KBG41)	- 6		A O O S		V					K S A E		
110653191065319	Phip 5	t est	g A	AFF S S	S. K.	4	11		74 V Y	4.	K T A F	GIA F P	EAX
tr 065320 065320 tr 065321 065321	Phip5			A		N.				A Y	100	GATE	EAX
tr 065318 065318	Phi p 5	E P			SXA	ΑE	1 -5 -6	L D A	(A V I	LAY	R THATE	GAT P	E A E
11P93467P93467 5pIP22284IMP91_POAPR	Phi p 5	EPK		ACAS		v.		U E A	4 Y	COLON Y	KTSE	GATE	
ap(Q40237)MP58_LOLPR			6 - Y	AD Q	34 38 N	0 333			33340X I 331		FASTO	G 20 1 1 1 1	EAK
triO9XF24jQ9XF24	Lolp 5A		36	A K A P		G	t P			3 V	W A A F K A G E	GATE	EAK
tri081343 081343	Lel p 50 Phl p 50206			- A P		. G 3922	V P 3@98			V	Ø102 A 2002 V	G AST	E A K
140239721023972	Hali5	;	🦋	T'KA,P		G	I PQ	N M	T: 1	TANK	AAAQ	GOAT P	EAK
1/1081344/081344 1/108434256/AAG42255	Phl p 5 0207 Hot 158			AQAP	1.1-1.	GF	V P	VAA	TS	AT	XAAV	C 4 1.0	T AVE
InjAAG42254JAAG42254	Pos p 5			AQAP		G F	V	VA	TS	AT	SSHEASHEV	G.A.T.P	E & K
1r 081342 081342 1r P93466 P93466	.PH p 5 0203 .PH p 5			A P		GILL	VP			V	KAAV AAV	647	
EPICHO963IMP5B_PHLPR	PH p 58		· : :	. A P		G	V P X	1000	A Y	VA	BAAV	GAT F	E O K
1/JQ9SBE0 Q9SBE0 1/JQ23971 Q23971	PN p 5.0204 PN p 5.02		14 m	ETKM	P	G L	S 33 25 25	嬢V D	Marg I	AAF		GATE	E A K
epIP56166IMP53_PHAAO	Pha e 5.3	. , . ,		STKG		1 1		LED A		VV	N TWA A	G A T P	F A K
HAAO HOO4828 004828	Pha a 5.1 Hor v 9	AAT	o i	GOSIS	MIL	K	KAR SSSS			Y A		G S	F A K
tr 039995 039995	Hor v S (30kDa)	1			35383 x 3532			Ø € L	2		D K Q	G.A. L.P.	EAX
					t								

FIG. 38B (Phl p 5)

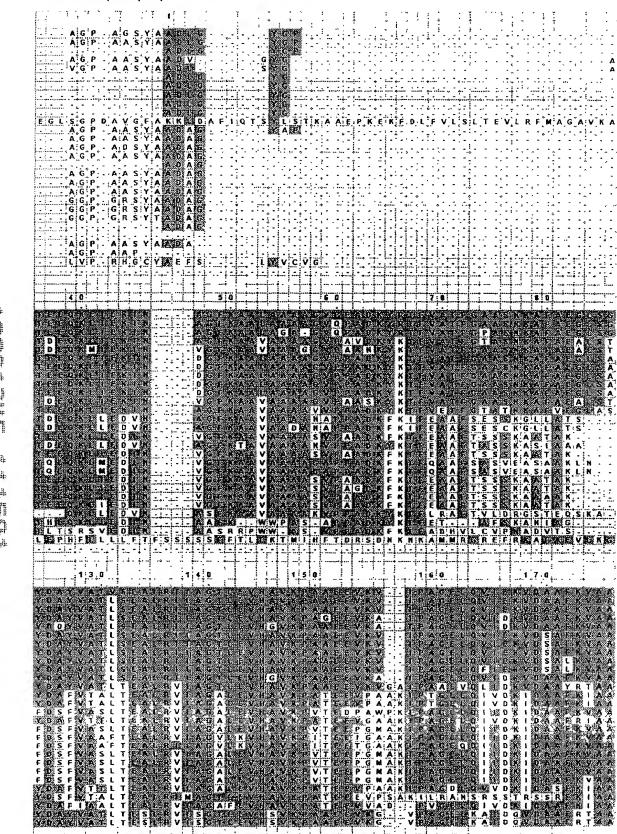
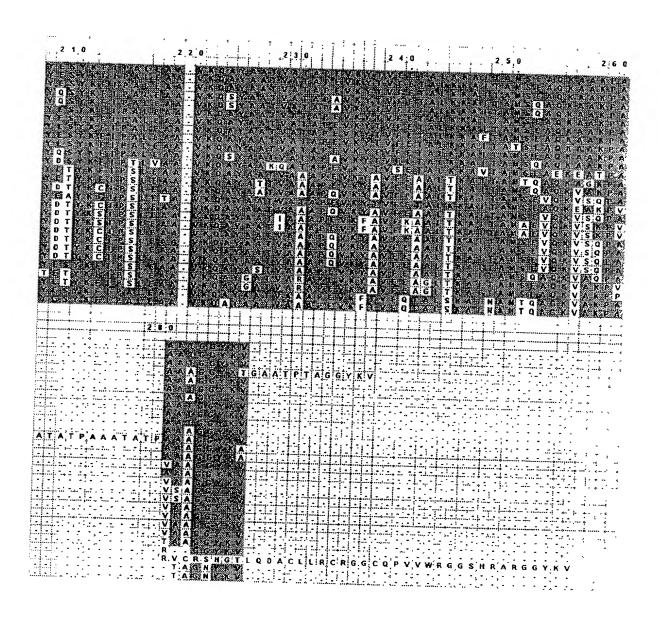


FIG. 38C (Phl p 5)

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1/10813411081341	Phi p 5.0103	L (TEACHTRACE FOR HID RESIDEN	THE BEAM OF HEAD AND A STREET A
triQ40960 Q40960	Phle5		DEA ALHA A PLANTORY DE	AND MARKET AND MEMBERS OF A STATE OF A
spiQ40962IMP5A_PHLPI spiP22285IMP92_POAPI		jaman, tarihinga kada kanadarihin		
spiP22286IMP93 POAPI				A CONTRACTOR OF THE PROPERTY O
11/065319(065319	Phi p 5			A A REAL NEW YORK AND A SECOND AND A SECOND ASSESSMENT AND A SECOND ASSESSMENT ASSESSMEN
11065320(065320	PN P.5	! ` -:-::- -:::::::::::::::::::::::::::::	THE AREA OF THE RESTRICT	FARTH NAME AS TO GA
1/10653211065321	Phi p 5		TARBARRANDET	PEANTRIALBASIGGA
tri065318j065318 triP93467jP93467	Phip5 Phip5			
spiP22284 MP91 POAPE				
splO40237 MP58_LOLPE	்ட் (நீ5 கீ் ்		TRABARRANDANT	FERTER NAME VELGAA
InQ9XF24 Q9XF24	Lol p 5A		TAANAAPT NORFES	FESIKENKALNECTOCA
tri095099 095099 tri081343 081343	Lat p 5C Phl p 5 0206	i dele, de suel geldi	A PART TRUSTER	E S A F H KIA LIK E CITE G A
1/10239721023972	Hol 15	I-1:5i1-5h1+1/14:H	ATAZAD	
1081344 061344	PN p 5 0207	7-1-1-1 1-1-1-1-1	SAVAIAITIA PAIDIEIELE	
tn/AAG42255/AAG42255	Hol 15B		THE TANK THE POLYMENT WITH THE	TENER KAN DE ESTE GA
tn/AAG42254/AAG42254 tr/O81342/O81342	Pos p 5		A A A A A A P A MUD AN STEE	E Con Cac A
tr[P93466[P93466	PN p 5 0203 PN p 5			
splO40963(MP6B_PHLPS	PN p 5B		THE ROOM THE A DE RICH	
triC9SBE0(C9SBE0	Phl p 5.0204		A A A T K ERA D D KEELS	AND
tr(023971 023971 sp PS6166IMPS3 PHAAC	Phi p 5.02 Pha e 5.3			AND I KNOW KELLEY KANGERSA
* HAYO	Pha # 5.3		<u>s</u>	G C K K K E R H C S P
ftr(004828)004828	Horv9		CHARLE D BY LATE TARE CONTROL	
140399991039995	Har v 5 (30kOs)	: 1-1-1-1-1-1-1-1-1	CHAPA D KAKHAMBADAKATAN	SLQQGPSRKPRCGA

	, ,,		270	damagna di adamata a mang la gara di antara di
triO813411O81341 triQ409601Q40960	Phip 5 0103			
spiQ40962jMP6A_PHLPR				
spiP22265[MP92_POAPR	Poa p 5 (KBG41)		. VIA TOTGA V.GA.E.	GAVGAATGAAT
spiP22286(MP93_POAPR			- R I G C A L SA VIS A C I	G A A T
triO65319(065319 triO65320(065320	PhipS	T'E'-	- A TABLE A TABLE A SECTION	
tr 065321 065321	PN 5	TE	- Caledon Aldon Side of Asset	
tr 065318 065318	:Phlp5	T.E	LA TRAITEAU A A A COA A SA	
tr P93467 P93467	PN p 5	TE		
spiP22284[MP91_POAPR spiO40237[MP5B_LOUPR	Poe p 5 (KBG 31) Lol p 5B		VIGIALSAVSA REPRESALATE	ATPAAAYATAAPAAAT
triQ9XF24jQ9XF24	Lol p 5A		A RU GIA DE VEIT E REAL	THE A A SHARE THE STATE OF THE
MGB2GB8(GB2GBB	: 6C واما:		AME GALLIVATE AME	A A A G G A H
tr 081343 081343 tr 023972 023972	Phi p 5.0206 Hol 15	T G	ADDIVAAGAATIATE	A.A.S S A.A.II
tr O81344 O81344	PN p 5 0207	T G		
InJAAG42255JAAG42255	Hol 158	. G	APO AATGAMATGAAAG	AATSAAU
tnIAAG42254JAAG42254	Pos p 5	GAATVAAG	ANDAATGAATGAAG	A A T A A A II
tri061342(081342 triP93466(P93466	PN p 5.0203 PN p 5	TG	A A VANGLATITA A G	A A S RANGE
sp(Q40963)MP58_PHLPR	PN p 5B	TG	A TVANGANTIN I G	A A S C A A S
14(09SBE0(Q9SBE0	PN p 5.0204	T G	A A U V A A G A A T T A B G	A A S D AAA T
11/023971/023971	Phi p 5 CO2	- A	Aleks and Line and Li	- VAADDAAL
BPIPSE166IMPS3_PHAAQ	Phs = 5.1	R L S P Q	P'P'Q'V'L P'L A GG A A	VAAASID S
tr 004828 004828	Hor v 9		A TANKET A V V A A C A A A	
tri0399961039995	Hor v 5 (30kDa)		- ATATAT VAAROAA	

FIG. 38D (Phl p 5)



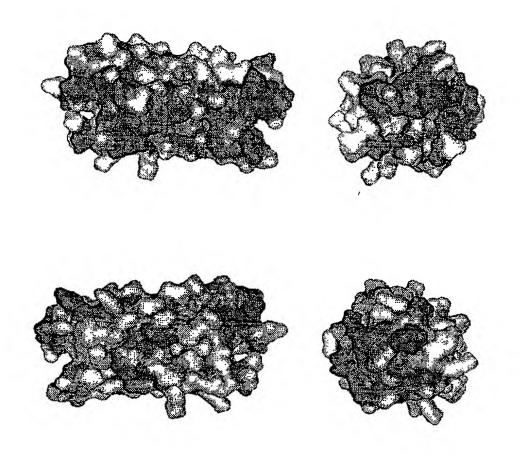


FIG. 39A: Phl p 5, Model A

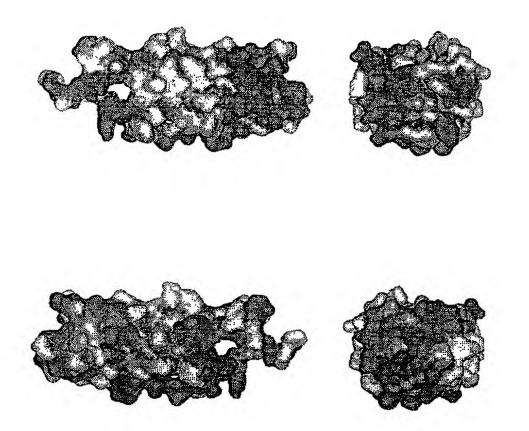


FIG. 39B: Phl p 5, Model B

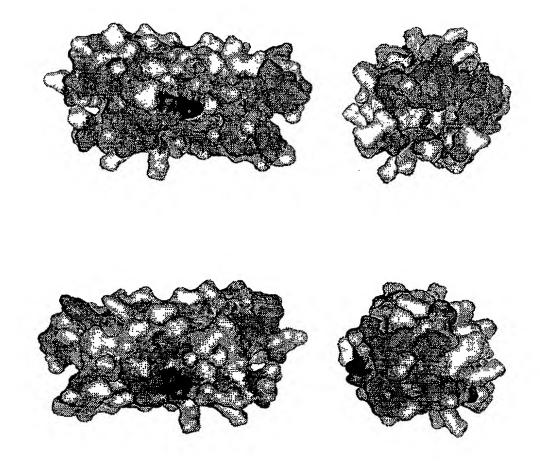


FIG. 40A: Phl p 5 mutant, Model A

j.

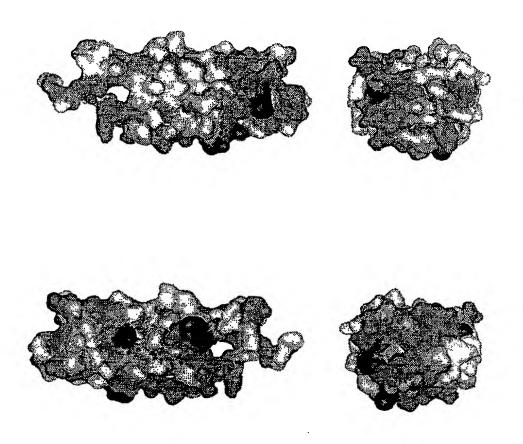


FIG. 40B: Phl p 5 mutant, Model B



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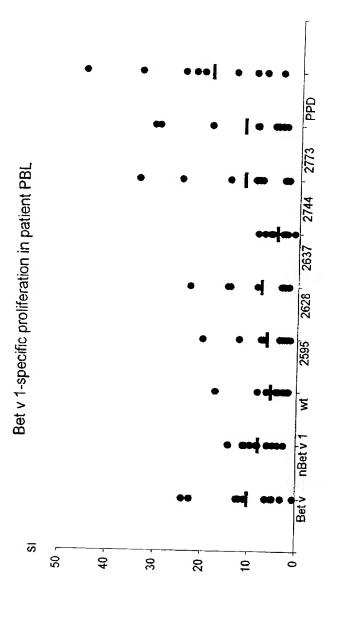
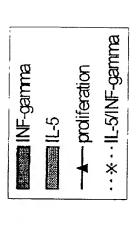
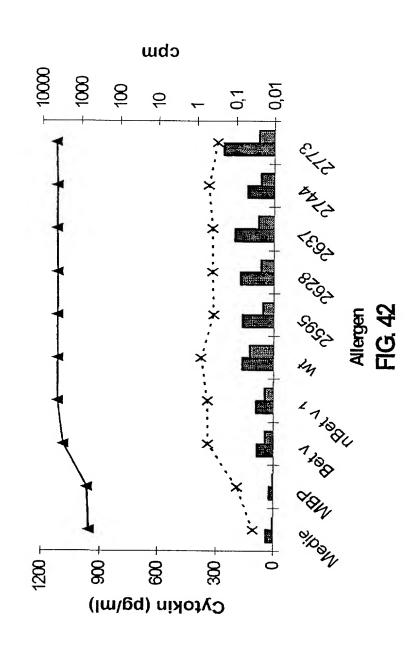


Figure 41: Stimulation of Bet v 1 samples





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